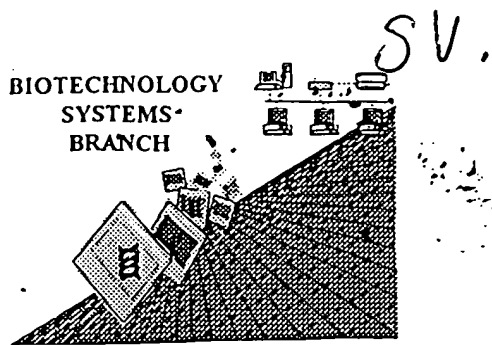


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/786635
Source: PCT 09
Date Processed by STIC: 11/14/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/786635

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(i) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(ii) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(x) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped.

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence.
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/786,635

DATE: 11/14/2001

TIME: 14:04:22

Input Set : A:\Lea33298.app

Output Set: N:\CRF3\11142001\I786635.raw

3 <110> APPLICANT: Bayer AG
 5 <120> TITLE OF INVENTION: ATP binding cassette genes and proteins for diagnosis
 6 and treatment of lipid disorders and inflammatory
 7 diseases
 9 <130> FILE REFERENCE: ATP binding cassette genes and protein
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/786,635 *OK*
 C--> 12 <141> CURRENT FILING DATE: 2001-03-07
 14 <150> PRIOR APPLICATION NUMBER: 101706
 15 <151> PRIOR FILING DATE: 1998-09-25
 17 <160> NUMBER OF SEQ ID NOS: 54
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 6880
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Human
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: cDNA of ABCA1 (ABCl)
 29 <400> SEQUENCE: 1
 30 caaacatgtc agctgttact ggaagtggcc tggcctctat ttatcttccct gatcctgatc 60
 31 tctgttccggc tgagctaccc accctatgaa caacatgaat gccattttcc aaataaagcc 120
 32 atgccctctg caggaacact tccttgggtt caggggatta tctgtaatgc caacaacccc 180
 33 tgtttccggt acccgactcc tggggaggct cccggagttg ttggaaactt taacaaatcc 240
 34 attgtggctc gcctgttctc agatgctcgg aggtctcttt tatacagcca gaaagacacc 300
 35 agcatgaagg acatgcgcaa agttctgaga acattacagc agatcaagaa atccagctca 360
 36 aacttgaagc ttcaagattt cctgggtggac aatgaaacct tctctgggtt cctgtatcac 420
 37 aacctctctc tcccaagtc tactgtggac aagatgctga gggctgatgt cattctccac 480
 38 aaggatattt tgcaaggcta ccagttacat ttgacaagtc tgtgcaatgg atcaaaatca 540
 39 gaagagatga ttcaacttgg tgaccaagaa gtttctgagc tttgtggcct accaagggag 600
 40 aaactggctg cagcagagcg agtacttctg tccaacatgg acatcctgaa gccaatcctg 660
 41 agaacactaa actctacatc tcccttcccg agcaaggagc tggccgaagc cacaaaaaca 720
 42 ttgctgcata gtcttgggac tctggcccag gagctgttca gcatgagaag ctggagtgc 780
 43 atgcgacagg aggtgatgtt tctgaccaat gtgaacagct ccagctctc caccctaatc 840
 44 taccaggctg tgtctcgtat tgtctgcggg catcccaggg gaggggggct gaagatcaag 900
 45 tctctcaact ggtatgagga caacaactac aaagccctct ttggaggcaa tggcactgag 960
 46 gaagatgctg aaaccttcta tgacaactct acaactcctt actgcaatga tttgatgaag 1020
 47 aatttgaggt ctagtccctt ttcccgcat atctggaaag ctctgaagcc gctgctcgtt 1080
 48 gggaagatcc tgtatacacc tgacactcca gccacaaggc aggtcatggc tgagggtgaac 1140
 49 aagaccttcc aggaactggc tgtgttccat gatctggaag gcatgtggga ggaactcagc 1200
 50 cccaagatct ggaccttcat ggagaacagc caagaaatgg acctgtccg gatgctgtt 1260
 51 gacagcaggg acaatgacca cttttgggaa cagcagttgg atggcttaga ttggacagcc 1320
 52 caagacatcg tggcgttttt ggccaagcac ccagaggatg tccagtccag taatggttct 1380
 53 gtgtacacct ggagagaagc ttccaacgag actaaccagg caatccggac catatctcgc 1440
 54 ttcatggagt gtgtcaacct gaacaagcta gaacctatg caacagaagt ctggctcatc 1500
 55 aacaagtcca tggagctgct ggtgagagga aagttctggg ctggtattgt gttcactgga 1560
 56 attactccag gcagcatgga gctgccccat catgtcaagt acaagatccg aatggacatt 1620
 57 gacaatgtgg agaggacaaa taaaatcaag gatgggtact gggaccctgg tccctcagct 1680
 58 gaccccttgg aggacatgcg gtacgtctgg gggggcttcg cctacttgca ggatgtgggt 1740

Does Not Comply
Corrected Diskette Needed

*Must enumerate unknown
See page 5 of 8 B*

RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/786,635

TIME: 14:04:22

Input Set : A:\Lea33298.app

Output Set: N:\CRF3\11142001\I786635.raw

```

59 gagcaggcaa tcatcagggt gctgacgggc accgagaaga aaactgggtgt ctatatgcaa 1800
60 cagatgcctt atccctgtta cgttgatgac atctttctgc gggatgatgag ccggtcaatg 1860
61 cccctcttca tgacgctggc ctggatttac tcagtggctg tgatcatcaa gggcatcgtg 1920
62 tatgagaagg aggcacggct gaaagagacc atgcggatca tgggcctgga caacagcatc 1980
63 ctctggttta gctggttcat tagtagcctc attcctcttc ttgtgagcgc tggcctgcta 2040
64 gtggtcatcc tgaagttagg aaacctgctg ccctacagtg atcccagcgt ggtgtttgtc 2100
65 ttctgtcccg tgtttgctgt ggtgacaatc ctgcagtgtc tcctgattag cacactcttc 2160
66 tccagagcca acctggcagc agcctgtggg ggcacatctt acttcacgct gtacctgccc 2220
67 tacgtcctgt gtgtggcatg gcaggactac gtgggcttca cactcaagat cttcgctagc 2280
68 ctgctgtctc ctgtggcttt tgggtttggc tgtgagtact ttgccctttt tgaggagcag 2340
69 ggcattggag tgcagtggga caacctgttt gagagtcctg tggaggaaga tggcttcaat 2400
70 ctaccactt cggctctccat gatgctgttt gacaccttc tctatgggtt gatgacctgg 2460
71 tacattgagg ctgtctttcc aggccagtag ggaattccca ggccctggta ttttcttgc 2520
72 accaagtcc actggttttg cgaggaaagt gatgagaaga gccacctgg ttccaaccag 2580
73 aagagaatat cagaaatctg catggaggag gaacccaccc acttgaagct gggcgtgtcc 2640
74 attcagaacc tggtaaaagt ctaccgagat gggatgaagg tggctgtcga tggcctggca 2700
75 ctgaattttt atgagggcca gatcacctcc ttcttgggcc acaatggagc ggggaagacg 2760
76 accaccatgt caatcctgac cgggttgttc ccccgacct cgggcaccgc ctacatcctg 2820
77 ggaaaagaca ttgcctctga gatgagcacc atccggcaga acctgggggt ctgtccccag 2880
78 cataacgtgc tgtttgacat gctgactgtc gaagaacaca tctggttcta tgcccgcttg 2940
79 aaagggctct ctgagaagca cgtgaaggcg gagatggagc agatggccct ggatgttgg 3000
80 ttgccatcaa gcaagctgaa aagcaaaaca agccagctgt cagggtggaat gcagagaaag 3060
81 ctatctgtgg ccttggcctt tgtcggggga tctaaggttg tcattctgga tgaaccaca 3120
82 gctggtgtgg acccttactc ccgcagggga atatgggagc tgctgtgaa ataccgaca 3180
83 ggccgcacca ttattctctc tacacaccac atggatgaag cggacgtcct gggggacagg 3240
84 attgccatca tctcccatgg gaagctgtgc tgtgtgggct cctccctgtt tctgaagaac 3300
85 cagctgggaa caggctacta cctgaccttg gtcaagaaag atgtggaatc ctccctcagt 3360
86 tctgcagaa acagtagtag cactgtgtca tacctgaaaa aggaggacag tgtttctcag 3420
87 agcagttctg atgtggcct gggcagcgac catgagagtg acacgctgac catcgatgtc 3480
88 tctgctatct ccaacctcat caggaagcat gtgtctgaag cccggctggt ggaagacata 3540
89 gggcatgagc tgacctatgt gctgccatat gaagctgcta aggaggagc ctttgtggaa 3600
90 ctctttcatg agattgatga ccggtcttca gacctgggca tttctagtta tggcatctca 3660
91 gagacgacct tggagaagaa attcctcaag gtggccgaag agagtgggtt ggatgctgag 3720
92 acctcagatg gtaccttgcc agcaagacga aacaggcggg ccttcgggga caagcagagc 3780
93 tgtcttcgcc cgttcactga agatgatgct gctgatccaa atgattctga catagacca 3840
94 gaatccagag agacagactt gctcagtggg atggatggca aagggtccta ccaggtgaaa 3900
95 ggtggaac ttacacagca acagtttgt gccctttgt ggaagagact gctaattgcc 3960
96 agacggagtc ggaaaggatt tttgtctcag attgtcttgc cagctgtgtt tgtctgcatt 4020
97 gcccttgtgt tcagcctgat cgtgccacc tttggcaagt accccagcct ggaacttcag 4080
98 ccctggatgt acaacgaaca gtacacattt gtcagcaatg atgtcctga ggacacggga 4140
99 acctggaac tottaaagc cctcaccaa gacctggct tcgggaccgc ctgtatggaa 4200
100 ggaaacccaa tccagacac gccctgccag gcaggggagg aagagtggac cactgcccc 4260
101 gttccccaga ccatcatgga cctcttcag aatgggaact ggacaatgca gaaccttca 4320
102 cctgcatgcc agtgtagcag cgacaaaatc aagaagatgc tgctgtgtg tccccagg 4380
103 gcaggggggc tgcctcctcc acaaagaaaa caaaacactg cagatatcct tcaggacctg 4440
104 acaggaagaa acatttcgga ttatctggtg aagacgtatg tgcagatcat agccaaaagc 4500
105 ttaaagaaca agatctgggt gaatgagttt aggtatggcg gctttccctt ggtgtcagt 4560
106 aatactcaag cacttctcct gagtcaagaa gttaatgatg ccaccaaaaa aatgaagaa 4620
107 cacctaaagc tggccaagga cagttctgca gatcgatttc tcaacagctt ggaagattt 4680

```

09786635-052201

RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/786,635

TIME: 14:04:22

Input Set : A:\Lea33298.app

Output Set: N:\CRF3\11142001\I786635.raw

108 atgacaggac tggacaccag aaataatgtc aaggtgtggt tcaataacaa gggctggcat 4740
 109 gcaatcagct ctttcttgaa tgtcatcaac aatgccattc tccgggccaa cctgcaaaag 4800
 110 ggagagaacc ctagccatta tgggaattact gctttcaatc atcccctgaa tctcaccaag 4860
 111 cagcagctct cagaggtggc tccgatgacc acatcagtggt atgtccttgt gtccatctgt 4920
 112 gtcatctttg caatgtcctt cgtcccagcc agctttgtcg tattcctgat ccaggagcgg 4980
 113 gtcagcaaaag caaaacacct gcagttcatc agtggagtga agcctgtcat ctactggctc 5040
 114 tctaattttg tctgggatat gtgcaattac gttgtccctg ccacactggg cattatcatc 5100
 115 ttcattctgt tccagcagaa gtccatgtgt tccctccacca atctgcctgt gctagccctt 5160
 116 ctacttttgc tgtatgggtg gtcaatcaca cctctcatgt acccagcctc ctttgtgttc 5220
 117 aagatcccca gcacagccta tgtgggtgtc accagcgtga acctcttcat tggcattaat 5280
 118 ggcagcgtgg ccacctttgt gctggagctg ttcaccgaca ataagctgaa taatatcaat 5340
 119 gatatactga agtccgtgtt cttgatcttc ccacattttt gcctgggacg agggctcatc 5400
 120 gacatggtga aaaaccaggc aatggctgat gccctggaaa ggtttgggga gaatcgcttt 5460
 121 gtgtcaccat tatcttggga cttggtggga cgaaacctct tcgccatggc cgtggaaggg 5520
 122 gtggtgttct tctcattac tgttctgac cagtacagat tcttcatcag gccagacct 5580
 123 gtaaatgcaa agctatctcc tctgaatgat gaagatgaag atgtgaggcg ggaaagacag 5640
 124 agaattcttg atggtggagg ccagaatgac atcttagaaa tcaaggagt gacgaagata 5700
 125 tatagaagga agcgggaagc tgcgtgtgac aggatttgcg tgggcattcc tctggtgag 5760
 126 tgctttgggc tctggtgagt taatggggtc ggaaaatcat caactttcaa gatgttaaca 5820
 127 ggagatacca ctgttaccag aggagattgt ttccttaaca gaaatagtat cttatcaaac 5880
 128 atccatgaag tacatcagaa catgggctac tgccctcagt ttgatgccat cacagagctg 5940
 129 ttgactggga gagaacacgt ggagttcttt gcccttttga gaggagtccc agagaaagaa 6000
 130 gttggcaagg ttggtgagtg ggcgattcgg aaactgggcc tcgtgaagta tggagaaaaa 6060
 131 tatgctggtg actatagtgg aggcacaaaa cgcaagctct ctacagccat ggctttgatc 6120
 132 ggcgggcctc ctgtggtgtt tctggatgaa cccaccacag gcatggatcc caaagcccgg 6180
 133 cggttcttgt ggaattgtgc cctaagtgtt gtcaaggagg ggagatcagt agtgcttaca 6240
 134 tctcatagta tggagaatg tgaagctctt tgcactagga tggcaatcat ggtcaatgga 6300
 135 aggttcaggt gccttggcag tgtccagcat ctaaaaaata ggtttggaga tggttataca 6360
 136 atagttgtac gaatagcagg gtccaacccg gacctgaagc ctgtccagga tttctttgga 6420
 137 cttgcatttc ctggaagtgt tccaaaagag aaacaccgga acatgctaca ataccagctt 6480
 138 ccatcttcat tatcttctct ggccaggata ttcagcatcc tctcccagag caaaaagcga 6540
 139 ctccacatag aagactactc tgtttctcag acaacacttg accaagtatt tgtgaacttt 6600
 140 gccaaggacc aaagtgatga tgaccactta aaagacctct cattacacaa aaaccagaca 6660
 141 gtagtggacg ttgcagttct cacatctttt ctacaggatg agaaagtga agaaagctat 6720
 142 gtatgaagaa tctgttcat acggggtggc tgaaagtaaa gagggactag actttccttt 6780
 143 gcaccatgtg aagtgttgtg gagaaaagag ccagaagttg atgtgggaag aagtaaactg 6840
 144 gatactgtac tgatactatt caatgcaatg caattcaatg 6880

146 <210> SEQ ID NO: 2

147 <211> LENGTH: 2201

148 <212> TYPE: PRT

149 <213> ORGANISM: Human

151 <220> FEATURE:

152 <223> OTHER INFORMATION: Peptide sequence of ABCA1 (ABC1)

154 <400> SEQUENCE: 2

155 Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn

156 1 5 10 15

158 Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly

159 20 25 30

161 Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp

RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/786,635

TIME: 14:04:22

Input Set : A:\Lea33298.app

Output Set: N:\CRF3\11142001\I786635.raw

```

162          35          40          45
164 Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp
165          50          55          60
167 Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser
168 65          70          75          80
170 Asn Leu Lys Leu Gln Asp Phe Leu Val Asp Asn Glu Thr Phe Ser Gly
171          85          90          95
173 Phe Leu Tyr His Asn Leu Ser Leu Pro Lys Ser Thr Val Asp Lys Met
174          100          105          110
176 Leu Arg Ala Asp Val Ile Leu His Lys Val Phe Leu Gln Gly Tyr Gln
177          115          120          125
179 Leu His Leu Thr Ser Leu Cys Asn Gly Ser Lys Ser Glu Glu Met Ile
180          130          135          140
182 Gln Leu Gly Asp Gln Glu Val Ser Glu Leu Cys Gly Leu Pro Arg Glu
183 145          150          155          160
185 Lys Leu Ala Ala Ala Glu Arg Val Leu Arg Ser Asn Met Asp Ile Leu
186          165          170          175
188 Lys Pro Ile Leu Arg Thr Leu Asn Ser Thr Ser Pro Phe Pro Ser Lys
189          180          185          190
191 Glu Leu Ala Glu Ala Thr Lys Thr Leu Leu His Ser Leu Gly Thr Leu
192          195          200          205
194 Ala Gln Glu Leu Phe Ser Met Arg Ser Trp Ser Asp Met Arg Gln Glu
195          210          215          220
197 Val Met Phe Leu Thr Asn Val Asn Ser Ser Ser Ser Ser Thr Gln Ile
198 225          230          235          240
200 Tyr Gln Ala Val Ser Arg Ile Val Cys Gly His Pro Glu Gly Gly Gly
201          245          250          255
203 Leu Lys Ile Lys Ser Leu Asn Trp Tyr Glu Asp Asn Asn Tyr Lys Ala
204          260          265          270
206 Leu Phe Gly Gly Asn Gly Thr Glu Glu Asp Ala Glu Thr Phe Tyr Asp
207          275          280          285
209 Asn Ser Thr Thr Pro Tyr Cys Asn Asp Leu Met Lys Asn Leu Glu Ser
210          290          295          300
212 Ser Pro Leu Ser Arg Ile Trp Lys Ala Leu Lys Pro Leu Leu Val
213 305          310          315          320
215 Gly Lys Ile Leu Tyr Thr Pro Asp Thr Pro Ala Thr Arg Gln Val Met
216          325          330          335
218 Ala Glu Val Asn Lys Thr Phe Gln Glu Leu Ala Val Phe His Asp Leu
219          340          345          350
221 Glu Gly Met Trp Glu Glu Leu Ser Pro Lys Ile Trp Thr Phe Met Glu
222          355          360          365
224 Asn Ser Gln Glu Met Asp Leu Val Arg Met Leu Leu Asp Ser Arg Asp
225          370          375          380
227 Asn Asp His Phe Trp Glu Gln Gln Leu Asp Gly Leu Asp Trp Thr Ala
228 385          390          395          400
230 Gln Asp Ile Val Ala Phe Leu Ala Lys His Pro Glu Asp Val Gln Ser
231          405          410          415
233 Ser Asn Gly Ser Val Tyr Thr Trp Arg Glu Ala Phe Asn Glu Thr Asn
234          420          425          430

```

09786635-052201

RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/786,635

TIME: 14:04:22

Input Set : A:\Lea33298.app

Output Set: N:\CRF3\11142001\I786635.raw

```

236 Gln Ala Ile Arg Thr Ile Ser Arg Phe Met Glu Cys Val Asn Leu Asn
237          435          440          445
239 Lys Leu Glu Pro Ile Ala Thr Glu Val Trp Leu Ile Asn Lys Ser Met
240          450          455          460
242 Glu Leu Leu Asp Glu Arg Lys Phe Trp Ala Gly Ile Val Phe Thr Gly
243 465          470          475          480
245 Ile Thr Pro Gly Ser Ile Glu Leu Pro His His Val Lys Tyr Lys Ile
246          485          490          495
248 Arg Met Asp Ile Asp Asn Val Glu Arg Thr Asn Lys Ile Lys Asp Gly
249          500          505          510
251 Tyr Trp Asp Pro Gly Pro Arg Ala Asp Pro Phe Glu Asp Met Arg Tyr
252          515          520          525
254 Val Trp Gly Gly Phe Ala Tyr Leu Gln Asp Val Val Glu Gln Ala Ile
255          530          535          540
257 Ile Arg Val Leu Thr Gly Thr Glu Lys Lys Thr Gly Val Tyr Met Gln
258 545          550          555          560
260 Gln Met Pro Tyr Pro Cys Tyr Val Asp Asp Ile Phe Leu Arg Val Met
261          565          570          575
263 Ser Arg Ser Met Pro Leu Phe Met Thr Leu Ala Trp Ile Tyr Ser Val
264          580          585          590
266 Ala Val Ile Ile Lys Gly Ile Val Tyr Glu Lys Glu Ala Arg Leu Lys
267          595          600          605
269 Glu Thr Met Arg Ile Met Gly Leu Asp Asn Ser Ile Leu Trp Phe Ser
270          610          615          620
272 Trp Phe Ile Ser Ser Leu Ile Pro Leu Leu Val Ser Ala Gly Leu Leu
273 625          630          635          640
275 Val Val Ile Leu Lys Leu Gly Asn Leu Leu Pro Tyr Ser Asp Pro Ser
276          645          650          655
278 Val Val Phe Val Phe Leu Ser Val Phe Ala Val Val Thr Ile Leu Gln
279          660          665          670
281 Cys Phe Leu Ile Ser Thr Leu Phe Ser Arg Ala Asn Leu Ala Ala Ala
282          675          680          685
284 Cys Gly Gly Ile Ile Tyr Phe Thr Leu Tyr Leu Pro Tyr Val Leu Cys
285          690          695          700
287 Val Ala Trp Gln Asp Tyr Val Gly Phe Thr Leu Lys Ile Phe Ala Ser
288 705          710          715          720
290 Leu Leu Ser Pro Val Ala Phe Gly Phe Gly Cys Glu Tyr Phe Ala Leu
291          725          730          735
293 Phe Glu Glu Gln Gly Ile Gly Val Gln Trp Asp Asn Leu Phe Glu Ser
294          740          745          750
296 Pro Val Glu Glu Asp Gly Phe Asn Leu Thr Thr Ser Val Ser Met Met
297          755          760          765
299 Leu Phe Asp Thr Phe Leu Tyr Gly Val Met Thr Trp Tyr Ile Glu Ala
300          770          775          780
302 Val Phe Pro Gly Gln Tyr Gly Ile Pro Arg Pro Trp Tyr Phe Pro Cys
303 785          790          795          800
305 Thr Lys Ser Tyr Trp Phe Gly Glu Glu Ser Asp Glu Lys Ser His Pro
306          805          810          815
308 Gly Ser Asn Gln Lys Arg Ile Ser Glu Ile Cys Met Glu Glu Glu Pro

```

09786635-052601

09/786635

Page 5 of 8B

<210> 3
<211> 1130
<212> DNA
<213> Human

<220>
<223> human cDNA of ABCB9

<400> 3
gccaatgncz cggtttcatc atggaactcc aggacggcta cagcacagag acaggggaga 60
agggcgccca gctgtcaggt ggccagaagc agcgggtggc catggccgng gctctggtgc 120
ggaaccccc agtcctcatc ctggatgaag ccaccagcgc tttggatgcc gagagcgagt 180
atctgatcca gcaggccatc catggcaacc tgtcagaagc acacggtact catcatcgcg 240
caccggctga gcaccgtgga gcacgcgcac ctcatgtgtg tgcctggaaa gggccgcgta 300
gtgcagcagg gcacccacca gcagcttgc tgcctcaggc cgggctttta cggcaagctn 360
gttgacgcgg cagatgtggg gtttcaaggc cgcagacttc acagctggcc acaacgagcc 420
tgtagccaac gggtcacaag gcctgatggg gggccctccc ttcgcccggg ggcagaggac 480
ccggtgcctg cctggcagat gtgcccacgg aggtttccag ctgcccctacc gagcccaggc 540
ctgcagcact gaaagacgac ctgccatgtc ccatgatacc cgttntgca atcttgcccc 600
tggtccctgc cccattccca gggcactctt acccennnct gggggatgtc caagagcata 660
gtcctctccc cataccctcc cagagaaggg gcttccctgt ccggagggag acacggggaa 720
cgggattttc cgtctctccc tcttgccagc tctgtgagtc tggccagggc gggtagggag 780
cgtggagggc atctgtctgc caattgcccg ctgccaatct aagccagtct cactgtgacc 840
acacgaaacc tcaactgggg gagtgaggag ctggccaggc ctggaggggc ctcaggtgcc 900
cccagcccg caccagctt tcgcccctcg tcaatcaacc cctggctggc agccgccctc 960
cccacaccgg cccctgtgct ctgctgtctg gaggccacgt ggaccttcac gagatgcatt 1020
ctcttctgtc tttggtggan gggatgggtc aaagcccagg atctggcttt gccagagggt 1080
gcaacatgtt gagagaaccc ggtcaataaa gtgtactacc tcttaccctt 1130

Unknown must be enumerated in fields
221, 222 and 223

Glokup

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

09786635.052201

VERIFICATION SUMMARY

DATE: 11/14/2001

PATENT APPLICATION: US/09/786,635

TIME: 14:04:23

Input Set : A:\Lea33298.app

Output Set: N:\CRF3\11142001\I786635.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:579 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:579 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:580 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:580 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:584 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:584 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:588 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:588 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:589 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:589 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:596 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:596 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:623 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:623 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:624 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:624 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:1205 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:1205 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:1205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1212 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:1212 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:1212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1213 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:1213 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:1213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1214 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:1214 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1577 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:1577 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:1577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1625 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:1625 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:1625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1720 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1720 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1986 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31

VERIFICATION SUMMARY

DATE: 11/14/2001

PATENT APPLICATION: US/09/786,635

TIME: 14:04:23

Input Set : A:\Lea33298.app

Output Set: N:\CRF3\11142001\I786635.raw

L:1986 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1988 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1988 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1988 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1990 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1990 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1993 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1993 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1994 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1994 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1995 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1995 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1995 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:2013 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:2013 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:2013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:2014 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:2014 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:2014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:2289 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:54
L:2289 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:54
L:2289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2291 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:54
L:2291 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:54
L:2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54